

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Coleman, Roger  
Bandman, Olga
- (ii) TITLE OF THE INVENTION: NOVEL HUMAN C5A-LIKE RECEPTOR
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Drive
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Herewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0198 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 415-855-0555
  - (B) TELEFAX: 415-845-4166
  - (C) TELEX:

(ii) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 333 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: Consensus
  - (B) CLONE: 346374
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Thr	Asn	Ser	Ser	Phe	Phe	Cys	Pro	Val	Tyr	Lys	Asp	Leu	Glu	Pro
1				5					10					15	
Phe	Thr	Tyr	Phe	Phe	Tyr	Leu	Val	Phe	Leu	Val	Gly	Ile	Ile	Gly	Ser
			20					25					30		
Cys	Phe	Ala	Thr	Trp	Ala	Phe	Ile	Gln	Lys	Asn	Thr	Asn	His	Arg	Cys
	35					40					45				
Val	Ser	Ile	Tyr	Leu	Ile	Asn	Leu	Leu	Thr	Ala	Asp	Phe	Leu	Leu	Thr
	50				55						60				
Leu	Ala	Leu	Pro	Val	Lys	Ile	Val	Val	Asp	Leu	Gly	Val	Ala	Pro	Trp
65				70					75					80	
Lys	Leu	Lys	Ile	Phe	His	Cys	Gln	Val	Thr	Ala	Cys	Leu	Ile	Tyr	Ile
			85					90						95	
Asn	Met	Tyr	Leu	Ser	Ile	Ile	Phe	Leu	Ala	Phe	Val	Ser	Ile	Asp	Arg
			100					105					110		
Cys	Leu	Gln	Leu	Thr	His	Ser	Cys	Lys	Ile	Tyr	Arg	Ile	Gln	Glu	Pro
	115						120					125			
Gly	Phe	Ala	Lys	Met	Ile	Ser	Thr	Val	Val	Trp	Leu	Met	Val	Leu	Leu
	130				135						140				
Ile	Met	Val	Pro	Asn	Met	Met	Ile	Pro	Ile	Lys	Asp	Ile	Lys	Glu	Lys
145				150						155				160	
Ser	Asn	Val	Gly	Cys	Met	Glu	Phe	Lys	Lys	Glu	Phe	Gly	Arg	Asn	Trp
			165					170						175	
His	Leu	Leu	Thr	Asn	Phe	Ile	Cys	Val	Ala	Ile	Phe	Leu	Asn	Phe	Ser
	180						185						190		
Ala	Ile	Ile	Leu	Ile	Ser	Asn	Cys	Leu	Val	Ile	Arg	Gln	Leu	Tyr	Arg
	195						200					205			
Asn	Lys	Arg	Asn	Ile	Asn	Tyr	Pro	Asn	Val	Lys	Lys	Ala	Leu	Ile	Asn
	210				215					220					
Ile	Leu	Leu	Val	Thr	Thr	Gly	Tyr	Ile	Ile	Cys	Phe	Val	Pro	Tyr	His
225				230						235				240	
Ile	Val	Arg	Ile	Pro	Tyr	Thr	Leu	Ser	Gln	Thr	Glu	Val	Ile	Thr	Asp
			245					250						255	
Cys	Ser	Thr	Arg	Ile	Ser	Leu	Phe	Lys	Ala	Lys	Glu	Ala	Thr	Leu	Leu
			260					265					270		
Leu	Ala	Val	Ser	Asn	Leu	Cys	Phe	Asp	Pro	Ile	Leu	Tyr	Tyr	His	Leu
	275					280						285			
Ser	Lys	Ala	Phe	Arg	Ser	Lys	Val	Thr	Glu	Thr	Phe	Ala	Ser	Pro	Lys
	290					295					300				
Glu	Thr	Lys	Ala	Gln	Lys	Gln	Lys	Leu	Arg	Cys	Glu	Asn	Asn	Ala	
305				310						315					

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1257 base pairs

(B) TYPE: coding

(C) STRANDEDNESS: single

(D) ORIENTATION: 5' to 3'

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 346874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGCTCATGC	TTCTCTGAAG	ACTTGCAGCA	AGGCTTGCTG	AGGCTCACAG	AAGATAGCCC	60
CAGTGTTTTG	GAGTGGTTTT	GAATGTGATT	CTGAGATCAG	ACTGACTGAG	CTGGAACTCCT	120
GGCTTTATAT	CTTACAGCT	ACWCAAGCTT	GGAGTCTTAG	AAATTTTTTC	TTTTCATTA	180
GCAGTCATCC	TTACTTTCCC	TCAAGATGAC	AAACAGTTCC	TTCTTCTGCC	CAGTTTATAA	240
AGATCTGGAG	CCATTCACGT	ATTTTTTTTA	TTTAGTTTTT	CTTGTGGGAA	TTATTGGAAG	300
TTGTTTTGCA	ACCTGGGCTT	TTATACAGAA	GAATACGAAT	CACAGGTGTG	TGAGCATCTA	360

CTTAAATTAAT	TTGCTTACAG	CCGATTTCCT	GCTTACTCTG	GCATTACCAG	TGAAAATTGT	420
TGTTGACTTG	GGTGTGGCAC	CTTGGAAACT	GAAGATATTC	CACTGCCAAG	TAACAGCCTG	430
CCTCATCTAT	ATCAATATGT	ATTTATCAAT	TATCTTCTTA	GCATTGTGCA	GCATTGACCG	540
CTGTCTTCAG	CTGACACACA	GCTGCAAGAT	CTACCGAATA	CAAGAACCOC	GGTTTGCCAA	600
AATGATATCA	ACCGTTGTGT	GGCTAATGGT	CCTTCTTATA	ATGGTGCCAA	ATATGATGAT	660
TCCCATCAAA	GACATCAAGG	AAAAGTCAAA	TGTGGGTTGT	ATGGAGTTTA	AAAAGGAATT	720
TGGAAGAAAT	TGGCATTTGC	TGACAAAATTT	CATATGTGTA	GCAATATTTT	TAAATTCTC	780
AGCCATCATT	TTAATATCCA	ATTGCGTTGT	AATTCGACAG	CTCTACAGAA	ACAAAGATAA	840
TGAAAATTAC	CCAAATGTGA	AAAAGGCTCT	CATCAACATA	CTTTTAGTGA	CCACGGGCTA	900
CATCAPATGC	TTTGTTCCTT	ACCACATTGT	CCGAATCCCG	TATACCCCTCA	GCCAGACAGA	960
AGTCATAACT	GATTGCTCAA	CCAGGATTTC	ACTCTTCAAA	GCCAAAGAGG	CTACACTGCT	1020
CCTGGCTGTG	TGGAACCTGT	GCTTTGATCC	TATCTGTGAC	TATCACCTCT	CAAAAGCATT	1080
CCGCTCAAA	GTCACGTAGA	CTTTTGCTTC	ACCTAAAGAG	ACCAAGGCTC	AGAAAGAAAA	1140
ATTAAGATGT	GAAAATAATG	CATAAAAGAC	AGGATTTTCT	GTGCTACCAA	TTCTGGGCTT	1200
ACTGGACCAT	AAAGTTAATT	ATAGCTTTGA	AAGATAAAAA	AAAAAAAAAA	AAAAAAA	1257

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 11525

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Asn	Ser	Phe	Asn	Tyr	Thr	Thr	Pro	Asp	Tyr	Gly	His	Tyr	Asp	Asp
1				5				10						15	
Lys	Asp	Thr	Leu	Asp	Leu	Asn	Thr	Pro	Val	Asp	Lys	Thr	Ser	Asn	Thr
			20					25					30		
Leu	Arg	Val	Pro	Asp	Ile	Leu	Ala	Leu	Val	Ile	Phe	Ala	Val	Val	Phe
		35					40					45			
Leu	Val	Gly	Val	Leu	Gly	Asn	Ala	Leu	Val	Val	Trp	Val	Thr	Ala	Phe
	50					55					60				
Glu	Ala	Lys	Arg	Thr	Ile	Asn	Ala	Ile	Trp	Phe	Leu	Asn	Leu	Ala	Val
65					70					75				80	
Ala	Asp	Phe	Leu	Ser	Cys	Leu	Ala	Leu	Pro	Ile	Leu	Phe	Thr	Ser	Ile
			85						90					95	
Val	Gln	His	His	His	Trp	Pro	Phe	Gly	Gly	Ala	Ala	Cys	Ser	Ile	Leu
	100							105					110		
Pro	Ser	Leu	Ile	Leu	Leu	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu	Leu	Ala
Thr	Ile	Ser	Ala	Asp	Arg	Phe	Leu	Leu	Val	Phe	Lys	Pro	Ile	Trp	Cys
Gln	Asn	Phe	Arg	Gly	Ala	Gly	Leu	Ala	Trp	Trp	Gln	Arg	His	Val	His
115			120						125					130	
Trp	Gly	Leu	Ala	Leu	Leu	Leu	Thr	Ile	Pro	Ser	Phe	Leu	Tyr	Arg	Val
			135						140					145	
Val	Arg	Glu	Glu	Tyr	Phe	Pro	Pro	Lys	Val	Leu	Cys	Gly	Val	Asp	Lys
			150						155					160	
Ser	His	Asp	Lys	Arg	Arg	Glu	Arg	Ala	Val	Ala	Ile	Val	Arg	Leu	Val
			165						170					175	
Leu	Gly	Phe	Leu	Trp	Pro	Leu	Leu	Thr	Leu	Thr	Ile	Cys	Tyr	Thr	Phe
	180								185					190	
Ile	Leu	Leu	Arg	Thr	Trp	Ser	Arg	Arg	Ala	Thr	Arg	Ser	Thr	Lys	Thr
225					230					235				240	
Leu	Lys	Val	Val	Val	Ala	Val	Val	Ala	Ser	Phe	Phe	Ile	Phe	Trp	Leu

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				245					250					255		
Pro	Tyr	Gln	Val	Thr	Gly	Ile	Met	Met	Ser	Phe	Leu	Glu	Pro	Ser	Ser	
			260					265					270			
Pro	Thr	Phe	Leu	Leu	Leu	Asn	Lys	Leu	Asp	Ser	Leu	Cys	Val	Ser	Phe	
		275					280					285				
Ala	Tyr	Ile	Asn	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Val	Val	Ala	Gly	
	290					295					300					
Gln	Gly	Phe	Gln	Gly	Arg	Leu	Arg	Lys	Ser	Leu	Pro	Ser	Leu	Leu	Arg	
305					310					315					320	
Asn	Val	Leu	Thr	Glu	Glu	Ser	Val	Val	Arg	Glu	Ser	Lys	Ser	Phe	Thr	
			325						330					335		
Arg	Ser	Thr	Val	Asp	Thr	Met	Ala	Gln	Lys	Thr	Gln	Ala	Val			
			340					345					350			